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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,370

DATE: 06/14/2001
TIME: 11:57:01

Input Set : N:\Crf3\RULE60\09852370.txt
Output Set: N:\CRF3\06142001\I852370.raw

3 <110> APPLICANT: Pomerantz, Joel L.
4 Sharp, Phillip A.
5 Pabo, Carl O.
7 <120> TITLE OF INVENTION: Chimeric DNA-binding proteins
9 <130> FILE REFERENCE: APV-022.02
12 <140> CURRENT APPLICATION NUMBER: 09/852,370
13 <141> CURRENT FILING DATE: 2001-05-10
15 <150> PRIOR APPLICATION NUMBER: 08/973,131
16 <151> PRIOR FILING DATE: 1997-11-26
18 <150> PRIOR APPLICATION NUMBER: PCT/US95/16982
19 <151> PRIOR FILING DATE: 1995-12-29
21 <150> PRIOR APPLICATION NUMBER: 08/366,083
22 <151> PRIOR FILING DATE: 1994-12-29
24 <160> NUMBER OF SEQ ID NOS: 75
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 26
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence:
35 oligonucleotide used to determine the consensus
36 binding sequence of ZFHD1
38 <400> SEQUENCE: 1
39 gtttggcacc tgactaattt aaggag 26
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 25
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Description of Artificial Sequence:
49 oligonucleotide used to determine the consensus
50 binding sequence of ZFHD1
52 <400> SEQUENCE: 2
53 gcgttaattt agggaggtttt ggcccc 25
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 25
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence:
63 oligonucleotide used to determine the consensus
64 binding sequence of ZFHD1
66 <400> SEQUENCE: 3
67 ctcggccgtt aatgagggtt gttcg 25
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 25

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72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Description of Artificial Sequence:
77 oligonucleotide used to determine the consensus
78 binding sequence of ZFHD1
80 <400> SEQUENCE: 4
81 taattatggg cgggatcgaa tagcc 25
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 26
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence:
91 oligonucleotide used to determine the consensus
92 binding sequence of ZFHD1
94 <400> SEQUENCE: 5
95 ggcaataatc aatcctttaa ttatgg 26
98 <210> SEQ ID NO: 6
99 <211> LENGTH: 26
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence:
105 oligonucleotide used to determine the consensus
106 binding sequence of ZFHD1
108 <400> SEQUENCE: 6
109 ggccgtacct catgaaattha gggcg 26
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 25
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:
119 oligonucleotide used to determine the consensus
120 binding sequence of ZFHD1
122 <400> SEQUENCE: 7
123 gttaattatg gggtaataat ggtgc 25
126 <210> SEQ ID NO: 8
127 <211> LENGTH: 25
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence:
133 oligonucleotide used to determine the consensus
134 binding sequence of ZFHD1
136 <400> SEQUENCE: 8
137 gtcgggctct gttaattatg ggtgg 25
140 <210> SEQ ID NO: 9

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141 <211> LENGTH: 25
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence:
147 oligonucleotide used to determine the consensus
148 binding sequence of ZFHD1
150 <400> SEQUENCE: 9
151 ggataattac gggtggcatt taggc 25
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 25
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence:
161 oligonucleotide used to determine the consensus
162 binding sequence of ZFHD1
164 <400> SEQUENCE: 10
165 gataaaatagg ggcgtcccat cccgt 25
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:
175 oligonucleotide used to determine the consensus
176 binding sequence of ZFHD1
178 <400> SEQUENCE: 11
179 taaatttaggg cttaattac ggtc 24
182 <210> SEQ ID NO: 12
183 <211> LENGTH: 25
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence:
189 oligonucleotide used to determine the consensus
190 binding sequence of ZFHD1
192 <400> SEQUENCE: 12
193 tcatttaggt gtaatgaga tgcgc 25
196 <210> SEQ ID NO: 13
197 <211> LENGTH: 26
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Description of Artificial Sequence:
203 oligonucleotide used to determine the consensus
204 binding sequence of ZFHD1
206 <400> SEQUENCE: 13
207 tagttgctaa tttgtattaa tttaag 26

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Input Set : N:\Crf3\RULE60\09852370.txt
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210 <210> SEQ ID NO: 14
211 <211> LENGTH: 25
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:
217 oligonucleotide used to determine the consensus
218 binding sequence of ZFHD1
220 <400> SEQUENCE: 14 25
221 agtattataat taagaatgtt aatta
224 <210> SEQ ID NO: 15
225 <211> LENGTH: 25
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:
231 oligonucleotide used to determine the consensus
232 binding sequence of ZFHD1
234 <400> SEQUENCE: 15 25
235 gtgtgataat gagctgggcc gtcccc
238 <210> SEQ ID NO: 16
239 <211> LENGTH: 25
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence:
245 oligonucleotide used to determine the consensus
246 binding sequence of ZFHD1
248 <400> SEQUENCE: 16 25
249 atattaaggc gtaattcggga caaga
252 <210> SEQ ID NO: 17
253 <211> LENGTH: 12
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
259 binding sequence of ZFHD1
261 <220> FEATURE:
262 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
264 <400> SEQUENCE: 17 12
W--> 265 taatttanggg ng
268 <210> SEQ ID NO: 18
269 <211> LENGTH: 12
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA
275 site
277 <220> FEATURE:

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Input Set : N:\Crf3\RULE60\09852370.txt
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278 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
280 <400> SEQUENCE: 18
W--> 281 **aatnnntggg cg** 12
284 <210> SEQ ID NO: 19
285 <211> LENGTH: 12
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: predicted
291 binding sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
296 <400> SEQUENCE: 19
W--> 297 **cgcannaa at** 12
300 <210> SEQ ID NO: 20
301 <211> LENGTH: 10
302 <212> TYPE: DNA
303 <213> ORGANISM: human
305 <400> SEQUENCE: 20
306 atgcaaatga 10
309 <210> SEQ ID NO: 21
310 <211> LENGTH: 12
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding
316 site
318 <400> SEQUENCE: 21
319 taatgatggg cg 12
322 <210> SEQ ID NO: 22
323 <211> LENGTH: 63
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding
329 site
331 <220> FEATURE:
332 <223> OTHER INFORMATION: "n" represents a, t, c, g or other
334 <400> SEQUENCE: 22
W--> 335 **ggctgagtct gaacggatcc nnnnnnnnnn nnnnnnnnnn nnnnnccctcg agactgagcg** 60
337 tcg 63
340 <210> SEQ ID NO: 23
341 <211> LENGTH: 12
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Description of Artificial Sequence: probe
348 <400> SEQUENCE: 23
349 tcattatggg cg 12

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/852,370

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Input Set : N:\Crf3\RULE60\09852370.txt
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L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:281 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:335 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:335 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:657 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:657 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:841 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:841 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:869 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:908 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:908 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: